## Protein synthesis

## Mark Scheme 2

| Level | International A Level |
| :--- | :--- |
| Subject | Biology |
| Exam Board | CIE |
| Topic | Nucleic acids and protein synthesis |
| Sub Topic | Protein synthesis |
| Booklet | Theory |
| Paper Type | Mark Scheme 2 |


| Time Allowed : | 66 minutes |  |
| :--- | :--- | :--- |
| Score |  | $/ 55$ |
| Percentage : | $/ 100$ |  |

Grade Boundaries:

| A $^{*}$ | A | B | C | D | E | U |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: |
| $>85 \%$ | $77.5 \%$ | $70 \%$ | $62.5 \%$ | $57.5 \%$ | $45 \%$ | $<45 \%$ |

1 (a D-uracil;
E-adenine ;
F - ribose ; I pentose / sugar
G - phosphate ; A phosphate
(b) answers must be in pairs

| mRNA | DNA |
| :--- | :--- |
| ribose | deoxyribose ; |
| differences between pentoses / sugar | may be described in terms of OH on C2 |
| uracil / no thymine | thymine / no uracil ; |
| single, polynucleotide / strand / chain | two, polynucleotides / chains / strands ; <br> A double |
| no hydrogen bonds | hydrogen bonding ; |
| not a helix / straight chain | (double) helix ; |
| ratio of A+G to C+T varies / AW | ratio of A+G to C+T = 1 / AW ; |
| no base pairing (within molecule) | base pairing ; |
| base pairing A-U with, tRNA / <br> anticodon | base pairing is A-T |
| shorter | longer ; |
| found in cytoplasm / leaves nucleus | found in nucleus ; |
| attached to ribosome(s) | not attached to ribosome(s) ; |
| short-lived | long-lived ; |
| transfer of information (to ribosome) | information storage / AW ; |
| codes for one polypeptide | codes for more than one polypeptide ; |
| produced by transcription | produced by (semi-conservative) <br> replication |

(c) 1 translation ; R if transcription given as well, unless in correct context A use of, nucleotide / base, sequence, to make, amino acid chain / polypeptide / protein I protein / polypeptide, synthesis moves towards / combines with, ribosome ;
3 ref to small and/or large sub-units ; I small / large ribosome
4 codon(s) ; only accept in correct context
5 transfer / t, RNA, bringing, amino acid(s), to mRNA / ribosome ;
6 anticodon(s) ; only accept in correct context
7 (complementary) base pairing ;
8 any e.g. of codon:anticodon base pairing ; need six bases
9 ref to polyribosome(s) / used by many ribosomes ;
10 (mRNA short-lived) ref to production of protein for short period of time ;

2 (a (i) A transcription;
B tRNA / transfer RNA;
C ribosome; A subunit of ribosome / ribosomal subunit treat 70S / 80S or small / large as neutral
D anticodon;
(ii) similarities
made of amino acids / amino acid monomers / polymer of amino acids A protein / polypeptides
have quaternary structure / have more than one polypeptide chain ;
four, sub-units / polypeptides;
haem / porphyrin / prosthetic group(s) ;
difference
(four) sub-units / polypeptides, are identical ;
or
haemoglobin has, two different, sub-units / polypeptides ;
or
haemoglobin has alpha and beta polypeptides ;
(catalase) has active site(s); A Hb has (oxygen) binding site
(iii) each, sub-unit / polypeptide, has an active site ;
catalase has four, active sites / haem groups ;
(b) iodine in potassium iodide solution / iodine in KI solution / I in KI solution; $\mathbf{A}$ iodine solution $\mathbf{R}$ iodine

Benedict's, solution / reagent; A Benedict's
A Fehling's solution / NaOH and $\mathrm{CuSO}_{4}$
treat refs to colour changes as neutral
[Total: 10]

## Question Expected Answers

(a) (i) A transcription; (ignore mRNA synthesis)

B translation;
C exocytosis; $\mathbf{R}$ secretion
(ii) D (sub unit of) ribosome

E Golgi apparatus/body;
(iii) $\mathbf{F} \quad \mathrm{mRNA}$;
(b) active site;
(is) specific shape; $\mathbf{A}$ complementary/other amino acids are the wrong shape to fit, $\mathbf{R}$ same shape
only accepts R groups of these two amino acids; $\mathbf{R}$ accepts peptide bond
(c) correct bond broken (between C-N);
involvement of water molecule in breaking the peptide bond shown clearly;
two amino acids with free groups as follows
$-\mathrm{COOH} /-\mathrm{COO}$ and $-\mathrm{NH}_{2} /-\mathrm{NH}_{3}{ }^{+}$;
A from diagram(s).
(b) accept glycine-valine or valine-glycine
peptide bond drawn correctly ;
amino and carboxylic acid ends shown ;
correct R-groups ;
water eliminated ;
(c) (i)

AAG $\} ;$
(ii) messenger;
(d) during systole semi-lunar valve is open ;
during diastole semi-lunar valve is closed;
proximity/AW pulmonary artery to (right) ventricle (so no pressure lost) ; elastic recoil of pulmonary artery maintains blood pressure/AW ; no/little blood in (right) ventricle, after contraction/during diastole ; fills with blood at low pressure ;
(e) increase in power of contraction ; AW increase in (systolic) blood pressure ; strain on right ventricle/right ventricle does not function efficiently ; growth of muscle in/right ventricle increases in thickness ; insufficient oxygen to, heart/cardiac, muscle ; heart failure/heart attack ;
(f) persistent/AW, cough ;
cough produces much mucus ;
wheezing;
rapid breathing/difficulty breathing/breathlessness ;
bluish colour to the skin ;
recurrent chest infections/frequent colds or flu/AW ;
barrel-shaped chest ;
chest pains; $\mathbf{R}$ heart pains
fatigue/weakness, (with exercise);

5 (a (i) GTG;
ACU ;
leu;
(ii) primary structure ;
(b) 1 mutation;

2 base substitution/T $\rightarrow A$ in template strand of DNA/AW ;
transcription
3 DNA has CAC as $6{ }^{\text {th }}$ triplet ;
4 (so) mRNA has GUG as ( $\left.6^{\text {th }}\right)$ codon ;
allow one mark for altered mRNA codon if no marks gained for mps 3 and 4

## translation

5 different tRNA involved/tRNA specific to val and not glu ;
6 anticodon on IRNA has CAC (with valine) ;
7 tRNA brings, incorrect amino acid/val, to ribosome ;
8 further detail ; e.g. incorrect amino acid incorporated into growing polypeptide chain

